

#16



SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> Helicobacter vaccine

<130> Degoedesequenties

<140>

<141>

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 2883

<212> DNA

<213> Helicobacter felis

<220>

<221> CDS

<222> (206)..(886)

<220>

<221> CDS

<222> (897)..(2603)

<400> 1

rggragattt tccarcactt caagcacata ttgatcctgt gttgtgggtg gtaaattrcr 60

acttgttaat rctattatta attttttaat aattacttat tatcatatat aataatatta 120

ttacttatat taaaaagtta ataaaaagta acgaaattag gactataatc ccattgcctt 180

taaaatttaa cacaaggagt aatag gtg aaa ctc aca ccc aaa gag caa gaa 232

Val Lys Leu Thr Pro Lys Glu Gln Glu

aag ttc ttg tta tat tat gcg ggc gaa gtg gct aga aag cgc aaa gca 280
Lys Phe Leu Leu Tyr Tyr Ala Gly Val Ala Arg Lys Arg Lys Ala
10 15 20 25

gag ggc tta aag ctc aac caa ccc gaa gcc att gct tac att agt gcc 328
Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala
30 35 40

cat att atg gac gaa gcg cgc cgt gga aaa aaa acc gtt gcc cag ctt 376
His Ile Met Asp Glu Ala Arg Arg Gly Lys Lys Thr Val Ala Gln Leu
45 50 55

atg gaa gag tgc atg cac ttt ttg aaa aaa gat gaa gta atg ccc ggg 424
Met Glu Glu Cys Met His Phe Leu Lys Lys Asp Glu Val Met Pro Gly
60 65 70

gtg ggt aat atg gtt ccc gat cta ggt gta gaa gcc acc ttt cct gat 472
Val Gly Asn Met Val Pro Asp Leu Gly Val Glu Ala Thr Phe Pro Asp
75 80 85

ggt acg aaa ctt gta act gtg aat tgg ccc atc gaa cca gat gag cac 520
Gly Thr Lys Leu Val Thr Val Asn Trp Pro Ile Glu Pro Asp Glu His
90 95 100 105

ttc aaa gcg ggc gaa gtg aaa ttt ggt tgc gat aaa gac atc gag ctc 568
Phe Lys Ala Gly Glu Val Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu
110 115 120

aat gca ggc aaa gaa gta acc gaa ctt gag gtt act aat gaa ggg cct 616
Asn Ala Gly Lys Glu Val Thr Glu Leu Glu Val Thr Asn Glu Gly Pro
125 130 135

aaa tcc ttg cat gtg ggt agc cat ttc cac ttc ttt gaa gct aac aag 664
Lys Ser Leu His Val Gly Ser His Phe His Phe Phe Glu Ala Asn Lys
140 145 150

gca cta aaa ttc gat cgt gaa aaa gcc tat ggc aaa cgc cta gat att 712

Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile
155 160 165

ccc tct ggc aac acg cta cgc att ggg gca gga caa acc cgc aaa gtg 760
Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala Gly Gln Thr Arg Lys Val
170 175 180 185

cag ttg att cct ctt ggt ggc agt aaa aaa gtg att ggc atg aac ggg 808
Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly
190 195 200

ctt gtg aat aac atc gcg gat gaa cgc cat aaa cat aaa gcg ctt gac 856
Leu Val Asn Asn Ile Ala Asp Glu Arg His Lys His Lys Ala Leu Asp
205 210 215

aag gcg aaa tct cac gga ttt atc aag taa ggagactccc atg aaa atg 905
Lys Ala Lys Ser His Gly Phe Ile Lys Met Lys Met
220 225 230

aaa aaa caa gaa tat gta aat acc tac gga ccc acc aaa ggc gat aaa 953
Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys Gly Asp Lys
235 240 245

gtg cgc tta gga gat acc gat ctt tgg gca gaa gta gaa cat gac tat 1001
Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu His Asp Tyr
250 255 260

acc acc tat ggc gaa gaa ctt aaa ttt ggc gcg ggt aaa act atc cgt 1049
Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg
265 270 275

gag ggt atg ggt cag agc aat agc cct gat gaa aac acc cta gat tta 1097
Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu
280 285 290

gtc atc act aac gcg atg att atc gac tac acc ggg att tac aaa gcc 1145
Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala
295 300 305 310

gac att ggg att aaa aac ggc aaa atc cat ggc att ggc aag gca gga			1193
Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly Lys Ala Gly			
315	320	325	
aac aag gac atg caa gat ⁷ ggc gta agc cct cat atg gtc gtg ggt gtg			1241
Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val Val Gly Val			
330	335	340	
ggc aca gaa gca cta gca ggg gaa ggt atg att att acc gct ggg gga			1289
Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr Ala Gly Gly			
345	350	355	
atc gat tca cac acc cac ttc ctt tct cca caa caa ttc cct acc gct			1337
Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala			
360	365	370	
cta gcc aat ggc gtt aca acc atg ttt gga ggc ggc aca ggt cct gta			1385
Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr Gly Pro Val			
375	380	385	390
gat ggc acg aat gcg act act atc act ccg ggc aaa tgg aac ttg cac			1433
Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp Asn Leu His			
395	400	405	
cgc atg ttg cgc gca gca gaa gag tat tct atg aat gtg ggc ttt ttg			1481
Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val Gly Phe Leu			
410	415	420	
ggc aaa ggc aat agc tct agc aaa aaa caa ctt gta gaa caa gta gaa			1529
Gly Lys Gly Asn Ser Ser Lys Lys Gln Leu Val Glu Gln Val Glu			
425	430	435	
gcg ggc gcg att ggt ttt aaa ttg cat gaa gac tgg ggc aca aca cca			1577
Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly Thr Thr Pro			
440	445	450	
agt gcg atc gat cac tgc ttg agc gtg gca gat gaa tac gat gtg caa			1625

Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr Asp Val Gln
455 460 465 470

gtt tgt atc cac acc gat aca gtc aat gag gca ggt tat gta gat gac 1673
Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr Val Asp Asp
475 480 485

acc cta aat gca atg aac ggg cgc gcc atc cat gcc tac cac att gag 1721
Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr His Ile Glu
490 495 500

gga gcg ggt gga gga cac tca cct gat gtt atc acc atg gca ggc gag 1769
Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met Ala Gly Glu
505 510 515

ctc aat att cta ccc tcc tcc acc acc ccc act att ccc tat acc att 1817
Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile
520 525 530

aat acg gtt gca gaa cac tta gac atg ctc atg aca tgc cac cac cta 1865
Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys His His Leu
535 540 545 550

gac aaa cgc atc cgc gag gat tta caa ttt tct caa agc cgt atc cgc 1913
Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg
555 560 565

ccc ggc tct atc gcg gct gaa gat gtg ctc cat gat atg ggt gtg atc 1961
Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met Gly Val Ile
570 575 580

gcg atg aca agc tcg gat tcg caa gca atg ggg cgt gca ggc gaa gtg 2009
Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala Gly Glu Val
585 590 595

att cct cga act tgg cag act gcg gat aag aat aaa aaa gaa ttt ggt 2057
Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly
600 605 610

aag ctt cct gaa gat ggc aaa gat aac gat aat ttc cgc att aag cgc 2105
Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg Ile Lys Arg
615 620 625 630

tac atc tcc aaa tac act atc aac ccc gct ttg acc cac ggc gtg agc 2153
Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His Gly Val Ser
635 640 645

gag tat atc ggc tct gtg gaa gag ggc aag atc gcc gac ttg gtg gtg 2201
Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp Leu Val Val
650 655 660

tgg aat cct gcc ttt ttt ggc gta aaa ccc aaa atc gtg atc aaa ggc 2249
Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val Ile Lys Gly
665 670 675

ggt atg gtg gtc ttc tct gaa atg ggc gat tct aac gcg tct gtg ccc 2297
Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala Ser Val Pro
680 685 690

act ccc caa ccg gtt tat tac cgc gaa atg ttt ggg cat cac ggc aag 2345
Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His His Gly Lys
695 700 705 710

gcg aaa ttt gac acc agc atc act ttt gtt tcc aaa gtc gcc tat gaa 2393
Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val Ala Tyr Glu
715 720 725

aat ggc gtg aaa gaa aag ctg ggc tta gag cgc caa gtt cta ccg gtc 2441
Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val Leu Pro Val
730 735 740

aaa aac tgc cgt aac atc acc aag aaa gac ttc aag ttc aac gac aaa 2489
Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe Asn Asp Lys
745 750 755

acg gca aaa atc acc gtc gat ccg aaa acc ttc gag gtc ttt gta gat 2537

Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val Phe Val Asp
760 765 770

ggc aaa ctc tgc acc tct aaa ccc acc tcg caa gtg cct cta gcc cag 2585
Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Gln Val Pro Leu Ala Gln
775 780 785 790

cgc tac act ttc ttc tag gcacaatgcc ccctttgggg gcagggttatt 2633
Arg Tyr Thr Phe Phe
795

ttaggaatct tcataaaacg cacctgcaat cggctttgcg tgtgcgatcg tgtcgctta 2693

aaacaacttt tcatctttaa gcaatcgcca ttttaatta atttaaattct tataaattaat 2753

attatattat gccccctcat ttttaaagga gaattatgcg taggtctttg gtattgctat 2813

gtgggggttg ttgggtgcctg ggccaaagg gtattgaaac ccatcgctc aaaaaagtag 2873

aagccacagg 2883

<210> 2
<211> 226
<212> PRT
<213> Helic

<400> 2
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
1 5 10 15

Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
 35 40 45

Arg Gly Lys Lys Thr Val Ala Gln Leu Met Glu Glu Cys Met His Phe

50 55 60
Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80
Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95
Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140
His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160
Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190
Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205
Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220
Ile Lys
225

<210> 3

<211> 568

<212> PRT

<213> Helicobacter felis

<400> 3

Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys
1 5 10 15

Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val

180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Gln Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe
565

<210> 4
<211> 2405
<212> DNA
<213> Helicobacter felis

<220>
<221> CDS
<222> (1)..(681)

<220>
<221> CDS
<222> (692)..(2398)

<400> 4
gtg aaa ctc aca ccc aaa gag caa gaa aag ttc ttg tta tat tat gcg 48
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
1 5 10 15

ggc gaa gtg gct aga aag cgc aaa gca gag ggc tta aag ctc aat caa 96
Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg cgc 144
Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

cgt ggc aaa aaa acc gtt gct gaa ctt atg gaa gaa tgt atg cac ttt 192
Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

ttg aaa aaa gat gag gtg atg ccc ggt gtg ggg aat atg gtc cct gat 240
Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

ttg ggc gta gaa gcc act ttc ccc gat ggc acc aaa ctc gta acc gtg 288
Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

aat tgg ccc att gaa cct gat gaa cac ttt aaa gcc ggt gaa gtg aaa		336
Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys		
100	105	110
ttt ggc tgt gat aaa gac att gag ctc aac gcg ggt aag gaa gtt acc		384
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr		
115	120	125
gag ctt gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc		432
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser		
130	135	140
cat ttc cac ttc ttt gaa acc aac aag gca ttg aaa ttc gat cg ^g gaa		480
His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu		
145	150	155
160		
aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta cgc		528
Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg		
165	170	175
att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggt		576
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly		
180	185	190
agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gcg gac		624
Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp		
195	200	205
gaa cgc cat aaa cac aaa gca cta gac aag gca aaa tct cac gga ttc		672
Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe		
210	215	220
atc aag taa ggagactccc atg aaa atg aaa aaa caa gag tat gta aac		721
Ile Lys	Met Lys Met Lys Lys Gln Glu Tyr Val Asn	
225	230	235
acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc gat		769
Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp		

240 245 250

ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag ctc 817
Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu
255 260 265

aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc aat 865
Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn
270 275 280 285

agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg att 913
Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile
290 295 300

atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat ggc 961
Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly
305 310 315

aaa atc cat ggt att ggc aag gcg ggg aac aaa gac atg caa gat ggc 1009
Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly
320 325 330

gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca ggg 1057
Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly
335 340 345

gaa ggt atg att att acc gct ggg ggg atc gat tcg cac acc cac ttc 1105
Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe
350 355 360 365

ctc tct ccc caa caa ttc cct acc gct cta gcc aat ggt gtt aca acc 1153
Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr
370 375 380

atg ttt gga ggt ggc aca ggt ccg gta gat ggc acg aat gcg acc acc 1201
Met Phe Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr
385 390 395

atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct gaa			1249
Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu			
400	405	410	
gag tat tct atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tcc agt			1297
Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser			
415	420	425	
aaa aaa caa ctc gta gaa caa gta gaa gcg ggc gcg att ggc ttt aaa			1345
Lys Lys Gln Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe Lys			
430	435	440	445
ttg cat gaa gac tgg ggc aca aca cca agt gcg atc gat cac tgc ttg			1393
Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu			
450	455	460	
agc gta gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat acg			1441
Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr			
465	470	475	
gtc aat gag gca ggt tat gta gat gac acc cta aat gcg atg aac ggg			1489
Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly			
480	485	490	
cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac tca			1537
Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly His Ser			
495	500	505	
cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc tcc			1585
Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser			
510	515	520	525
acc acc ccc act att ccc tat acc att aat acg gtt gca gaa cac tta			1633
Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu			
530	535	540	
gac atg ctc atg acc tgc cac cac cta gac aaa cgc atc cgc gag gat			1681
Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp			

545	550	555	
ctc cag ttt tcc caa agc cgt atc cgc ccc ggc tct att gcc gct gaa 1729			
Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu			
560	565	570	
gat gtg ctc cat gat att ggc gtg atc gcg atg aca agc tcg gat tcg 1777			
Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser			
575	580	585	
caa gca atg ggg cgc gct ggg gaa gtg att cct aga act tgg caa act 1825			
Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr			
590	595	600	605
gca gac aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt gca 1873			
Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala			
610	615	620	
gat aat gac aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc att 1921			
Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile			
625	630	635	
aat ccc gct ttg acc cat ggc gtg agc gag tat atc ggc tct gtg gaa 1969			
Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu			
640	645	650	
gag ggc aag atc gcc gac ttg gtg gtg tgg aat cct gct ttc ttt ggt 2017			
Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly			
655	660	665	
gta aaa ccc aaa atc gtg atc aaa ggc ggt atg gtg gtg ttc tct gaa 2065			
Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu			
670	675	680	685
atg ggc gat tct aac gcg tct gtg ccc aca cct cag ccg gtt tat tac 2113			
Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr			
690	695	700	

cgc gaa atg ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc	2161		
Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile			
705	710	715	
act ttt gtt tcc aaa gtc gcc tat gaa aat ggc gtg aaa gaa aaa cta	2209		
Thr Phe Val Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu			
720	725	730	
ggc tta gag cgc aag gtg cta ccc gtg aaa aac tgc cgc aac atc act	2257		
Gly Leu Glu Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr			
735	740	745	
aag aaa gac ttc aaa ttc aac aac aag acg gcg cat atc act gtc gat	2305		
Lys Lys Asp Phe Lys Phe Asn Asn Lys Thr Ala His Ile Thr Val Asp			
750	755	760	765
cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa	2353		
Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys			
770	775	780	
ccc gcc tct gaa gtg cct cta gcc caa cgc tac act ttc ttc tag	2398		
Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe			
785	790	795	
gcacaat	2405		

<210> 5
<211> 226
<212> PRT
<213> Helicobacter felis

<400> 5			
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala			
1	5	10	15
Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln			
20	25	30	

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys

<210> 6
<211> 568
<212> PRT
<213> *Helicobacter felis*

<400> 6
 Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
 1 5 10 15

 Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
 20 25 30

 His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
 35 40 45

 Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
 50 55 60

 Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
 65 70 75 80

 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
 85 90 95

 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
 100 105 110

 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
 115 120 125

 Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
 130 135 140

 Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
 145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala

355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro³⁷⁵ Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Ala Ser Glu Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe

565

<210> 7

<211> 2183

<212> DNA

<213> Helicobacter felis

<220>

<221> CDS

<222> (3)..(683)

<220>

<221> CDS

<222> (694)..(2181)

<400> 7

tc gtg aaa ctc aca ccc aaa gag caa gaa aag ttc ttg tta tat tat 47
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr
1 5 10 15

gct ggc gaa gtg gct aga aag cgc aaa gca gag ggc tta aag ctc aat 95
Ala Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn
20 25 30

caa ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gct 143
Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala
35 40 45

cgc cgt ggc aaa aaa acc gtt gct gaa ctt atg gaa gaa tgt atg cac 191
Arg Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His
50 55 60

ttt ttg aaa aaa gat gag gtg atg ccc ggt gtg ggg aat atg gtc cct 239
Phe Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro
65 70 75

gat ttg ggc gta gaa gcc act ttc ccc gat ggc acc aaa ctc gta acc			287
Asp Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr			
80	85	90	95
gtg aat tgg ccc att gaa ² cct gat gaa cac ttt aaa gcc ggt gaa gtg			335
Val Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val			
100	105	110	
aaa ttt ggc tgt gat aaa gac att gag ctc aac gtg ggt aag gaa gtt			383
Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Val Gly Lys Glu Val			
115	120	125	
acc gag ctt gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt			431
Thr Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly			
130	135	140	
agc cat ttc cac ttc ttt gaa acc aac aag gca ttg aaa ttc gat cgg			479
Ser His Phe His Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg			
145	150	155	
gaa aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta			527
Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu			
160	165	170	175
cgc att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc			575
Arg Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly			
180	185	190	
ggt agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gcg			623
Gly Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala			
195	200	205	
gac gaa cgc cat aaa cac aaa gca cta gac aag gca aaa tct cac gga			671
Asp Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly			
210	215	220	
ttc atc aag taa ggagactccc atg aaa atg aaa aaa caa gag tat gta			720

Phe Ile Lys	Met Lys Met Lys Lys Gln Glu Tyr Val	
225	230	235
aac acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc		768
Asn Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr		
240	245	250
gat ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag		816
Asp Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu		
255	260	265
ctc aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc		864
Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser		
270	275	280
aat agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg		912
Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met		
285	290	295
att atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat		960
Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn		
305	310	315
ggc aaa atc cat ggt att ggc aag gcg ggg aac aaa gac atg caa gat		1008
Gly Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp		
320	325	330
ggc gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca		1056
Gly Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala		
335	340	345
ggg gaa ggt atg att att acc gct ggg ggg atc gat tcg cac acc cac		1104
Gly Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His		
350	355	360
ttc ctc tct ccc caa caa ttc cct acc gct cta gcc aat ggt gtt aca		1152
Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr		
365	370	375
		380

acc atg ttt gga ggt ggc aca ggt ccg gta gat ggc acg aat gcg acc 1200
Thr Met Phe Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr
385 390 395

acc atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct 1248
Thr Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala
400 405 410

gaa gag tat tct atg aat gta ggc ttt ttg ggc aaa ggc aat agt tct 1296
Glu Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser
415 420 425

agc aaa aaa caa ctt gta gaa caa gta gaa gcg ggc gcg att ggc ttt 1344
Ser Lys Lys Gln Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe
430 435 440

aaa ttg cat gaa gac tgg ggc aca aca cca agt gcg atc gat cac tgc 1392
Lys Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys
445 450 455 460

ttg agc gtg gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat 1440
Leu Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp
465 470 475

acg gtc aat gag gca ggt tat gtg gat gac acc cta aat gca atg aac 1488
Thr Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn
480 485 490

ggg cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac 1536
Gly Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly His
495 500 505

tca cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc 1584
Ser Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser
510 515 520

tcc acc acc ccc act att ccc tat acc att aat acg gtt gca gaa cac 1632

Ser	Thr	Thr	Pro	Thr	Ile	Pro	Tyr	Thr	Ile	Asn	Thr	Val	Ala	Glu	His	
525																540
tta gac atg ctc atg acc tgc cac cac cta gat aag cgc atc cgc gag															1680	
Leu	Asp	Met	Leu	Met	Thr	Cys	His	His	Leu	Asp	Lys	Arg	Ile	Arg	Glu	
																555
gat tta caa ttt tct caa agc cgt atc cgc ccc gga tct att gcc gct															1728	
Asp	Leu	Gln	Phe	Ser	Gln	Ser	Arg	Ile	Arg	Pro	Gly	Ser	Ile	Ala	Ala	
																560
565															570	
gag gat gtg ctc cat gat att ggc gtg atc gcg atg act agc tcc gat															1776	
Glu	Asp	Val	Leu	His	Asp	Ile	Gly	Val	Ile	Ala	Met	Thr	Ser	Ser	Asp	
																575
580															585	
tcg caa gca atg ggg cgc gct ggg gaa gtg att cct aga act tgg caa															1824	
Ser	Gln	Ala	Met	Gly	Arg	Ala	Gly	Glu	Val	Ile	Pro	Arg	Thr	Trp	Gln	
																590
595															600	
act gca gat aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt															1872	
Thr	Ala	Asp	Lys	Asn	Lys	Glu	Phe	Gly	Lys	Leu	Pro	Glu	Asp	Gly		
																605
610															620	
gca gat aac gac aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc															1920	
Ala	Asp	Asn	Asp	Asn	Phe	Arg	Ile	Lys	Arg	Tyr	Ile	Ser	Lys	Tyr	Thr	
																625
630															635	
att aat ccc gct ttg acc cat ggc gtg agc gag tat atc ggc tct gtg															1968	
Ile	Asn	Pro	Ala	Leu	Thr	His	Gly	Val	Ser	Glu	Tyr	Ile	Gly	Ser	Val	
																640
645															650	
gaa gag ggc aag atc gcc gac ttg gtg gtg tgg aat cct gcc ttt ttt															2016	
Glu	Glu	Gly	Lys	Ile	Ala	Asp	Leu	Val	Val	Trp	Asn	Pro	Ala	Phe	Phe	
																655
660															665	
ggc gtg aaa cct aag att gtg att aaa ggt ggc atg gtg gtc ttc tct															2064	
Gly	Val	Lys	Pro	Lys	Ile	Val	Ile	Lys	Gly	Gly	Met	Val	Val	Phe	Ser	
																670
675															680	

gaa atg ggc gat tct aac gcg tcc gtg ccc acg cct cag ccg gtt tat 2112
Glu Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr
685 690 695 700

tac cgc gaa atg ttt ggg cac cac ggc aag gcg aaa ttt gac acc agc 2160
Tyr Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser
705 710 715

atc act ttt cgt gtc tca agc gg 2183
Ile Thr Phe Arg Val Ser Ser
720

<210> 8
<211> 226
<212> PRT
<213> Helicobacter felis

<400> 8
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
1 5 10 15

Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Val Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys
225

<210> 9
<211> 496
<212> PRT
<213> Helicobacter felis

<400> 9

Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
1 5 10 15

Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu

20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Arg Val Ser Ser
485 490 495

<210> 10

<211> 2407

<212> DNA

<213> Helicobacter felis

<220>

<221> CDS

<222> (2)..(682)

<220>

<221> CDS

<222> (693)..(2399)

<400> 10

c gtg aaa ctc aca ccc aaa gag caa gaa aag ttc ttg tta tat tat gcg 49
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
1 5 10 15

ggc gaa gtg gct aga aag cgc aaa gcg gag ggc tta aag ctc aac caa 97
Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg cgc 145

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg				
35	40	45		
cgt ggc aaa aag acc gtt gcg gaa ctt atg gaa gag tgt atg cac ttt 193				
Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe				
50	55	60		
ttg aaa aaa gac gag gtg atg ccc ggt gtg ggg aat atg gtc cct gat 241				
Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp				
65	70	75	80	
tta ggc gtg gaa gct act ttt ccc gat ggc acc aaa ctc gta acc gtg 289				
Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val				
85	90	95		
aat tgg ccc atc gaa ccc gat gaa cac ttc aaa gcg ggc gaa gtc aaa 337				
Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys				
100	105	110		
ttt ggc tgt gat aaa gac att gaa ctc aac gca ggt aag gaa gtt acc 385				
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr				
115	120	125		
gaa cta gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc 433				
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser				
130	135	140		
cat ttc cac ttc ttt gaa gcc aac aag gca ttg aaa ttc gat cgg gaa 481				
His Phe His Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu				
145	150	155	160	
aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta cgc 529				
Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg				
165	170	175		
att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggc 577				
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly				
180	185	190		

agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gca gat 625
Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

gaa cgc cat aaa cac aaa qcg tta gaa aaa gca aaa tct cac gga ttt 673
Glu Arg His Lys His Lys Ala Leu Glu Lys Ala Lys Ser His Gly Phe
210 215 220

atc aaa taa ggagactccc atg aaa atg aaa aaa caa gag tat gta aat 722
Ile Lys Met Lys Met Lys Gln Glu Tyr Val Asn
225 230 235

acc tac gga cct acc aca ggc gac aaa gtg cgc tta gga gat acc gat 770
Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp
240 245 250

ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag ctc 818
Leu Trp Ala Glu Val Glu His Asp Tyr Thr Tyr Gly Glu Glu Leu
255 260 265

aaa ttt ggc gcg ggt aaa act atc cgt gag ggc atg ggt cag agc aat 866
Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn
270 275 280 285

agt cca gat gaa aac acc cta gat tta gtc atc acc aac gcg atg att 914
Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile
290 295 300

att gac tac acc ggg att tac aaa gcc gac att ggc att aaa aat ggc 962
Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly
305 310 315

aaa atc cat ggc att ggc aag gca gga aac aag gac atg caa gat ggc 1010
Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly
320 325 330

gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca tta gca ggg 1058

Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly
335 340 345

gaa ggt atg att att acc gct ggg ggg atc gat tca cac acc cac ttc 1106
Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe
350 355 360 365

ctc tct cca caa caa ttc cct acc gct cta gcc aat ggc gtt aca acc 1154
Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr
370 375 380

atg ttt ggc ggt ggc aca ggt ccg gta gat ggc acg aat gcg act acc 1202
Met Phe Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr
385 390 395

atc act ccg ggc aaa tgg aac ttg cac ccg atg ttg ccg gca gct gaa 1250
Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu
400 405 410

gag tat tct atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tcc agt 1298
Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser
415 420 425

aaa aaa caa ctt gta gaa caa ata gaa gcg ggc gcg atc ggc ttt aaa 1346
Lys Lys Gln Leu Val Glu Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys
430 435 440 445

ttg cat gaa gac tgg ggc aca act cca agt gca atc gat cac tgc ttg 1394
Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu
450 455 460

agc gta gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat acg 1442
Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr
465 470 475

gtc aat gag gca ggt tat gta gat gac acc ctg aat gcg atg aac ggg 1490
Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly
480 485 490

cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac tca		1538
Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly His Ser		
495	500	505
cct gat gtt atc acc atg ⁷ gca ggc gag ctc aat att cta ccc tcc tcc		1586
Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser		
510	515	520
525		
aca acc ccc act atc ccc tat acc att aat acg gtt gca gaa cac tta		1634
Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu		
530	535	540
540		
gac atg ctc atg acc tgc cac cac cta gat aaa cgc atc cgc gag gat		1682
Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp		
545	550	555
555		
tta caa ttt tcc caa agc cgt atc cgc ccc ggc tct atc gcc gct gaa		1730
Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu		
560	565	570
570		
gat gtg ctc cat gat att ggc gtg atc gcg atg aca agc tcg gat tcg		1778
Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser		
575	580	585
585		
caa gca atg ggg cgc gct ggc gaa gtg att cct cga act tgg cag act		1826
Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr		
590	595	600
605		
gcg gat aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat agt gca		1874
Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala		
610	615	620
620		
gat aac gac aac ttc cgt atc aaa cgc tac atc tcc aaa tac act att		1922
Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile		
625	630	635
635		
aac ccc gct cta acc cat ggg gta agc gag tat atc ggc tct gtg gaa		1970

Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu			
640	645	650	
gag ggc aaa atc gct gat ttg gtg gtg tgg aat cct gcc ttt ttt ggt 2018			
Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly			
655	660	665	
gtg aaa cct aag att gtg atc aaa ggc ggt atg gtg gtc ttc tct gaa 2066			
Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu			
670	675	680	685
atg ggc gac tcc aac gcg tcc gtg cct aca cct cag ccg gtt tat tac 2114			
Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr			
690	695	700	
cgc gaa atg ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc 2162			
Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile			
705	710	715	
act ttt gtt tcc aaa gtc gcc tat gaa aat ggc gtg aaa gaa aaa cta 2210			
Thr Phe Val Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu			
720	725	730	
ggc tta gag cgc aag gtg cta ccc gtg aaa aac tgc cgc aac atc act 2258			
Gly Leu Glu Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr			
735	740	745	
aag aaa gac ttc aaa ttc aac aac aag acg gcg cat atc act gtc gat 2306			
Lys Lys Asp Phe Lys Phe Asn Asn Lys Thr Ala His Ile Thr Val Asp			
750	755	760	765
cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa 2354			
Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys			
770	775	780	
ccc gcc tct gaa gtg cct cta gcc cag cgc tac act ttc ttc tag 2399			
Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe			
785	790	795	

gcncaatg

2407

<210> 11
<211> 226
<212> PRT
<213> Helicobacter felis

<400> 11
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
1 5 10 15

Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu

145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Glu Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys

225

<210> 12

<211> 568

<212> PRT

<213> Helicobacter felis

<400> 12

Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
1 5 10 15

Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met

275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Ala Ser Glu Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe
565

<210> 13
<211> 2452
<212> DNA
<213> Helicobacter felis

<220>
<221> CDS
<222> (48)..(728)

<220>
<221> CDS
<222> (739)..(2445)

<400> 13
aggactataa tcccatcgcc tttaaaattt aacacaagga gtaatag gtg aaa ctc 56
Val Lys Leu
1

aca ccc aaa gag caa gaa aag ttc ttg tta tat tat gcg ggc gaa gtg 104
 Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val
 5 10 15

gct aga aag cgc aaa gca gag ggc tta aag ctc aac caa ccc gaa gcc 152
 Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala
 20 25 30 35

att gcc tac att agt gcc cat att atg gac gag gcg cgt cgt ggc aaa 200
 Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg Arg Gly Lys
 40 45 50

aaa acc gtt gcg gaa ctt atg gaa gag tgt atg cac ttt ttg aaa aaa 248
 Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe Leu Lys Lys
 55 60 65

gac gag gtg atg ccc ggg gtg ggg aat atg gtc cct gat ttg ggc gtg 296
 Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp Leu Gly Val
 70 75 80

gaa gcc act ttc ccc gat ggc acc aaa ctc gta act gtg aat tgg ccc 344
 Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val Asn Trp Pro
 85 90 95

atc gaa cct gat gaa cac ttt aag gcg ggt gaa gtg aaa ttt ggc tgt 392
 Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys Phe Gly Cys
 100 105 110 115

gat aaa gac att gaa ctc aac gca ggt aag gaa gtt acc gaa cta gaa 440
 Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr Glu Leu Glu
 120 125 130

gtt act aac gaa gga cct aaa tcc ttg cat gtg ggt agc cat ttc cac 488
 Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser His Phe His
 135 140 145

ttc ttt gaa gcc aac aaa gca ttg aaa ttc gat cggt gaa aaa gcc tat 536
 Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr

150 155 160
ggc aaa cgc cta gat att ccc tct ggc aac aca cta cgc att ggg gca 584
Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala
165 170 175
gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggt agt aaa aaa 632
Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys
180 185 190 195
gtg att ggc atg aac ggg ctt gtg aat aat att gcg gac gaa cgc cat 680
Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp Glu Arg His
200 205 210
aaa cac aaa gcg cta gac aaa gca aaa tct cac gga ttt atc aag taa 728
Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe Ile Lys
215 220 225
ggagactccc atg aaa atg aaa aaa caa gag tat gta aat acc tac gga 777
Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly
230 235 240
ccc acc aca ggc gat aaa gtg cgc tta gga gat acc gat ctt tgg gca 825
Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala
245 250 255
gaa gta gaa cat gac tat acc acc tat ggc gaa gaa ctc aaa ttc ggt 873
Glu Val Glu His Asp Tyr Thr Tyr Gly Glu Glu Leu Lys Phe Gly
260 265 270
gca ggt aaa act atc cgt gag ggt atg ggt cag agc aat agc cca gat 921
Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp
275 280 285
gaa aac acc tta gat tta gtg atc acc aac gcg atg att att gac tac 969
Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr
290 295 300

acc ggg att tac aaa gcc gac att ggc att aaa aat ggc aaa atc cat 1017
 Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His
 305 310 315 320

ggc att ggc aag gca gga aac aag gac atg caa gat ggc gta agc cct 1065
 Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro
 325 330 335

cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca ggg gaa ggt atg 1113
 His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met
 340 345 350

att att acc gct ggg ggg atc gat tca cac acc cac ttc ctc tct cca 1161
 Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro
 355 360 365

caa caa ttc cct acc gct cta gcc aat ggc gtt aca aca atg ttt ggc 1209
 Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly
 370 375 380

ggt ggc aca ggc ccc gta gat ggc acg aat gcg act acc atc act ccg 1257
 Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro
 385 390 395 400

ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gca gaa gag tat tct 1305
 Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser
 405 410 415

atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tct agt aaa aaa caa 1353
 Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln
 420 425 430

ctt gta gaa caa gta gaa gcg ggc gcg att ggt ttt aaa ttg cat gaa 1401
 Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu
 435 440 445

gac tgg ggc aca act cca agt gcg atc gat cac tgc ttg agc gta gca 1449
 Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala

450 455 460
gat gaa tac gat gtg caa gtt tgt ata cac acc gat acg gtc aat gag 1497
Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu
465 470 475 480

gca ggt tat gta gat gac acc cta aat gca atg aac ggg cgc gcc atc 1545
Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile
485 490 495

cat gcc tac cac att gag gga gcg ggt gga gga cac tca cct gat gtt 1593
His Ala Tyr His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val
500 505 510

atc acc atg gca ggc gaa gtg aat att cta ccc tcc tcc aca acc cct 1641
Ile Thr Met Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro
515 520 525

act atc ccc tat acc att aat acg gtt gca gaa cac tta gac atg ctt 1689
Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu
530 535 540

atg acc tgc cac cac cta gat aaa cgc atc cgc gag gat ctccaa ttt 1737
Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe
545 550 555 560

tct caa agc cgt atc cgc ccc ggc tct atc gcc gct gaa gat gtg ctc 1785
Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu
565 570 575

cat gat atc ggt gtg atc gcg atg aca agt tcc gat tcg caa gca atg 1833
His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met
580 585 590

ggg cgc gct ggg gaa gtg att cct aga act tgg caa act gca gac aag 1881
Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys
595 600 605

aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt gca gat aat gac			1929
Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp			
610	615	620	
aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc att aat ccc gct			1977
Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala			
625	630	635	640
ttg acc cat ggc gtg agc gag tat atc ggc tct gtg gaa gag ggc aag			2025
Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys			
645	650	655	
atc gcc gac ttg gtg tgg aat cct gcc ttt ttt ggc gta aaa ccc			2073
Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro			
660	665	670	
aaa atc gtg atc aaa ggc ggt atg gtg gtg ttc tct gaa atg ggc gat			2121
Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp			
675	680	685	
tct aat gcg tct gtg ccc act cct cag ccg gtt tat tac cgc gaa atg			2169
Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met			
690	695	700	
ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc act ttt gtt			2217
Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val			
705	710	715	720
tcc aaa gtc gcc tat gaa aat ggt gtg aaa gaa aaa cta ggt tta gag			2265
Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu			
725	730	735	
cgc aag gtg ctc ccc gtg aaa aac tgc cgt aac atc acc aag aag gac			2313
Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp			
740	745	750	
ttc aag ttc aac gac aaa act gca aaa atc acc gtc gat ccg aaa acc			2361
Phe Lys Phe Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr			

755

760

765

ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa ccc acc tct 2409
Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser
770 775 780

gaa gtg cct cta gcc caa cgc tac act ttc ttc tag gcataat 2452
Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe
785 790 795

<210> 14

<211> 226

<212> PRT

<213> Helicobacter felis

<400> 14

Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
1 5 10 15

Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys
225

<210> 15
<211> 568
<212> PRT
<213> Helicobacter felis

<400> 15
Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
1 5 10 15

Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys

35

40

45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Glu Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe
565

<210> 16
<211> 21
<212> DNA
<213> Helicobacter felis

<400> 16
catgcacttt ttgaaaaaaag a 21

<210> 17
<211> 16

<212> DNA
<213> Helicobacter felis

<400> 17
tatgggtggtc ttctct

16

<210> 18
<211> 32
<212> DNA
<213> Helicobacter felis

<400> 18
ggagtaacat atgaaactca cacccaaaga gc

32

<210> 19
<211> 27
<212> DNA
<213> Helicobacter felis

<400> 19
cacacccacg accatgtgag ggcttac

27

<210> 20
<211> 27
<212> DNA
<213> Helicobacter felis

<400> 20
gtaaggccctc acatggtcgt gggtgtg

27

<210> 21
<211> 34
<212> DNA
<213> Helicobacter felis

<400> 21

cgaattcgg a tcctagaaga aagtgtacg ctgg

34